

```

1  MVRSGNKA AVL CMDV GFTMSNSIPGIESPFEQAKKVITMFVQRQVFAEN 50
  |||||||
1  MVRSGNKA AVL CMDV GFTMSNSIPGIESPFEQAKKVITMFVQRQVFAEN 50
  |||||||
51 KDEIALVLF GDTGNPLSGDQYQNTVHRHMLPDPFDLLEDIESKIQP 100
  |||||||
51 KDEIALVLF GDTGNPLSGDQYQNTVHRHMLPDPFDLLEDIESKIQP 100
  |||||||
101 GSQQADFLDALIVSMDVIQHETICKKFEKRHIEFTDLSSRFSKSQLDII 150
  |||||||
101 GSQQADFLDALIVSMDVIQHETICKKFEKRHIEFTDLSSRFSKSQLDII 150
  |||||||
151 IHSLKKCDISLQFFLPFSLGKEDGSGDRGDGPPRLGGHGSPFLKGITEQ 200
  |||||||
151 IHSLKKCDISLQFFLPFSLGKEDGSGDRGDGPPRLGGHGSPFLKGITEQ 200
  |||||||
201 QKEGLEIVKMVMISLEGEDGLDEIYFSFESLRKLCVFKKIERHSIHWPGR 250
  |||||||
201 QKEGLEIVKMVMISLEGEDGLDEIYFSFESLRKLCVFKKIERHSIHWPGR 250
  |||||||

```

Fig. 1

```

251 LTIGSNLSTRIAAYKSIQERVKKTWTVVDKTLKKEDIQETVYCLNDD 300
|||||
251 LTIGSNLSTRIAAYKSIQERVKKTWTVVDKTLKKEDIQETVYCLNDD 300
|||||
301 DETEVLKEDIQGFYGSDIVPFSKVDEEQMKYKSEGKCFSVLGFCCKSSQ 350
|||||
301 DETEVLKEDIQGFYGSDIVPFSKVDEEQMKYKSEGKCFSVLGFCCKSSQ 350
|||||
351 VQRRFFMGNOVLKVFAARDEAAAVALSLSLIHALDDLDMVAIVRYAYDKR 400
|||||
351 VQRRFFMGNOVLKVFAARDEAAAVALSLSLIHALDDLDMVAIVRYAYDKR 400
|||||
401 ANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQ 450
|||||
401 ANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQ 450
|||||
451 INAVDALIDMSLAKKDEKDTLEDLFPTTKIPNPRFQRLFQ 492
|||||
451 INAVDALIDMSLAKKDEKDTLEDLFPTTKIPNPRFQRLFQ 492

```

Fig. 1 (Cont.)

1 MVRSGNKAADVLCMDVGTMTNSIPGIESPFQAKKVTIMFVQRQVFAEN 50  
 1 MVRSGNKAADVLCMDVGTMTNSIPGIESPFQAKKVTIMFVQRQVFAEN 50  
 51 KDEIALVLFGTGDTNPLSGGDQYQNTIVHRHMLPDEFDLEDIESKIQP 100  
 51 KDEIALVLFGTGDTNPLSGGDQYQNTIVHRHMLPDEFDLEDIESKIQP 100  
 101 GSQQADFLDALIVSMDVIQHETIGKKFEKRHIEFTDLSSRFSKSQLDII 150  
 101 GSQQADFLDALIVSMDVIQHETIGKKFEKRHIEFTDLSSRFSKSQLDII 150  
 151 IHSKKKCDISIQFFLPFSLGKEDSGDRGDGPFRLGGHGSPFPLKGITEQ 200  
 151 IHSKKKCDISIQFFLPFSLGKEDSGDRGDGPFRLGGHGSPFPLKGITEQ 200  
 201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKLGVFKKIERHSIHWPGR 250  
 201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKLGVFKKIERHSIHWPGR 250

Fig. 2.

251 LTIGSNLSIRIAAYKSIQERVKKTWVVDATAKLKKEDIQKETVYCLNDD 300  
 |||||  
 251 LTIGSNLSIRIAAYKSIQERVKKTWVVDATAKLKKEDIQKETVYCLNDD 300  
 301 DETE..... 304  
 ||||  
 301 DETEVLKEDIQGFYRGSDIVPFKVDDEEQMKYSEKCFSVLGFCKSSQ 350  
 305 .....LNPPAEVTTKSQIPLSKIKITLPLIEAKKKDQVTA 339  
 |||||  
 501 PRELPPIQQHIWNMLNPPAEVTTKSQIPLSKIKITLPLIEAKKKDQVTA 550  
 340 QEIFQDNHEDGPTAKKLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 389  
 |||||  
 551 QEIFQDNHEDGPTAKKLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 600  
 390 LVKQKKASFEASNLINHIETQFLDTNETPYFMKSIDCIRAFREEAIKFS 439  
 |||||  
 601 LVKQKKASFEASNLINHIETQFLDTNETPYFMKSIDCIRAFREEAIKFS 650

Fig. 2 (Cont.)

```

440 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGTILITKEEASGSSVTAE 489
      |||||
651 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGTILITKEEASGSSVTAE 700
      |||||

      .
      490 AKKFLAPKDKPSGDTAAVFEEGGDVDDLLDMI 521
            |||||
      701 AKKFLAPKDKPSGDTAAVFEEGGDVDDLLDMI 732
            |||||

```

Fig. 2 (Cont.)

Fig. 3

252 GAGQFGEVWMGYNGHTKVAVKSLKQGSMPDAFLAEANIMKQLQHQLV 301  
 |||||  
 251 GAGQFGEVWMGYNGHTKVAVKSLKQGSMPDAFLAEANIMKQLQHQLV 300  
 |||||  
 302 RLYAVVTQEPYIITEYMEENGSLVDFLKTPSGIKLTINKLLDMAAQIAEG 351  
 |||||  
 301 RLYAVVTQEPYIITEYMEENGSLVDFLKTPSGIKLTINKLLDMAAQIAEG 350  
 |||||  
 352 MAFIERNYIHRDLRAANILVSDTLCKTADFGLARLIEDIHHQVR 397  
 ||||| : |  
 351 MAFIERNYIHRDLRAANILVSDTLCKTADFGLARLIEDNEYTAR 396

Fig. 3 (Cont.)

[illegible]

**Fig. 4 (Cont.)**



```

2  GCGSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVY 51
   |||||
1  GCGSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVY 50
   |||||
52 EGSNPPASPIQDPQQGLKDKACGSLAVGFHLSPTYFLPGLAFLVPHPV 101
   |||||
51 EGSNPPASPIQ..... 61
102 TPGFIPIPARFSLTPLVFTDNLVIALHSYEPSHDGDLGFEKGEQLRILEQ 151
   |||||
62 .....DNLVIALHSYEPSHDGDLGFEKGEQLRILEQ 92
152 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEPWFKNLSRKDAERQLLA 201
   |||||
93 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEPWFKNLSRKDAERQLLA 142
202 PGNTHGSFLIRESESTAGSFSLSVRDFDQNGGEVVKHYKIRNLNNGGFYI 251
   |||||
143 PGNTHGSFLIRESESTAGSFSLSVRDFDQNGGEVVKHYKIRNLNNGGFYI 192
252 SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTKPKPWWEDWEVPRE 301
   |||||
193 SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTKPKPWWEDWEVPRE 242

```

Fig. 4

[illegible]

```

62 AEAIPCTLAVSNPHTDAWKSHGLVEVASYCEESRGNNQWVPYISLQER 109
   | : | | |.||||| | | | | | | | | | | | | | | | | | | |
114 ARDLHC.LLVTNPHTDAWKSHGLVEVASYCEESRGNNQWVPYISLQER 160

```

**Fig. 6**

```

1 MRAPPQVCEALLFALALQTGVCYGIKWLALSKTPSALALNQTQHCCKQLEG 50
  |||||
1 MRARPQVCEALLFALALQTGVCYGIKWLALSKTPSALALNQTQHCCKQLEG 50
  |||||
51 LVSAQVQLCRSNLELMHTVVHAAAREVMKACRRAFADMRWNCSSIELAPNY 100
  |||||
51 LVSAQVQLCRSNLELMHTVVHAAAREVMKACRRAFADMRWNCSSIELAPNY 100
  |||||
101 LLDLERTRESAFVYALSAATISHAIAIACTSGDLPGCSCGPVPGPPGP 150
  |||||
101 LLDLERTRESAFVYALSAATISHAIAIACTSGDLPGCSCGPVPGPPGP 150
  |||||
151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKMLRLHNSVEVGRQA 200
  |||||
151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKMLRLHNSVEVGRQA 200
  |||||
201 LRASLEMKCKHGVSGSCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250
  |||||
201 LRASLEMKCKHGVSGSCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250
  |||||

```

Fig. 7

```

251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN 300
|||||
251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN 300
|||||
301 KTSNGSDSCDLM.....CCVYTCRRCERTVER 327
|||||
301 KTSNGSDSCDLMCCGRGNPYTDVRVERCHCKYHWCCYVTCRRCERTVER 350
|||||
328 YVCK 331
|||||
351 YVCK 354

```

**Fig. 7 (Cont.)**

1 MRARPQVCEALLFALALQTGVCYGIKWLALSKTPSALALNQTQHCKQLEG 50  
 |||||  
 1 MRARPQVCEALLFALALQTGVCYGIKWLALSKTPSALALNQTQHCKQLEG 50  
 |||||  
 51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100  
 |||||  
 51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100  
 |||||  
 101 LLDLERTRESAFVYA..... 116  
 |||||  
 101 LLDLERTRESAFVYALSAATISHAIARACTSGDLPGCSCGPVPEPPGP 150  
 |||||  
 117 .....AADLKTRYLSATKVVHR 133  
 |||||  
 201 LRASLEMKCKCHGVSGCSIRTCWKLQELQDVAADLKTRYLSATKVVHR 250  
 |||||  
 134 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN 183  
 |||||  
 251 PMGTRKHLVPKDLDIRPVKDWELVYLQSSPDFCMKNEKVGSHGTQDRQCN 300  
 |||||

Fig. 8

184 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 233  
 |||||  
 301 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 350

234 YVCK 237

||||

351 YVCK 354

**Fig. 8 (Cont.)**

```

1 MSPFLRIGLSNFDGSCQCGEAVNPYCAVLKVEYVESENGOMYIQKP 50
  |||||
1 MSPFLRIGLSNFDGSCQCGEAVNPYCAVLKVEYVESENGOMYIQKP 50
  |||||

51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLSETTVELYSLAERCCKNN 100
  |||||
51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLSETTVELYSLAERCCKNN 100
  |||||

101 GKTEIWLELKPQGRMLMNARYFTLEMSDTKDMNEFETEGFFALHQRRGAIK 150
  |||||
101 GKTEIWLELKPQGRMLMNARYFTLEMSDTKDMNEFETEGFFALHQRRGAIK 150
  |||||

151 QAKVHHVKCHEFTATFFPQPTFCSVCHEFVWGLNKQGYQCRQCNAAIHKK 200
  |||||
151 QAKVHHVKCHEFTATFFPQPTFCSVCHEFVWGLNKQGYQCRQCNAAIHKK 200
  |||||

201 CIDKVIACKTGSAINSRFTMFHKERFKIDMPHRFKVINYKSPTFCEHCGT 250
  |||||
201 CIDKVIACKTGSAINSRFTMFHKERFKIDMPHRFKVINYKSPTFCEHCGT 250
  |||||

251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINOKLMAEALAMISTQQ 300
  |||||
251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINOKLMAEALAMISTQQ 300
  |||||

```

Fig. 9



```

301 ARCLRDTEQIFREGPVEIGLPCSIKNEARPPCLPTPGKREPQGISWESPL 350
    |||||
301 ARCLRDTEQIFREGPVEIGLPCSIKNEARLPCPTPGKREPQGISWESPL 350
    |||||
351 DEVDRMCHLPEPELNKERPSIQIKLIEDFILHKMLGKSGFGKVFLAEFK 400
    |||||
351 DEVDRMCHLPEPELNKERPSIQIKLIEDFILHKMLGKSGFGKVFLAEFK 400
    |||||
401 KTNQFFAIKALKKDVLMDDVECTMVEKRVLSLAWEHFELTHMFCFTQT 450
    |||||
401 KTNQFFAIKALKKDVLMDDVECTMVEKRVLSLAWEHFELTHMFCFTQT 450
    |||||
451 KENLFFVMEYLNCGDIMYHIQSKHKFDLSRATFYAAEIIIGLQFLHSGKI 500
    |||||
451 KENLFFVMEYLNCGDIMYHIQSKHKFDLSRATFYAAEIIIGLQFLHSGKI 500
    |||||
501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550
    |||||
501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550
    |||||

```

Fig. 9 (Cont.)

```

551 LLGQYNHSDWWSFGVLLYEMLLIGQSPFHGQDEEELFHSIRMDNPFYPR 600
    |||||
551 LLGQYNHSDWWSFGVLLYEMLLIGQSPFHGQDEEELFHSIRMDNPFYPR 600
    |||||

601 WLEKEAKDLLVKV 613
    |||||
601 WLEKEAKDLLVKL 613

```

Fig. 9(Cont.)

[illegible]

**Fig. 10**

[illegible]

**Fig. 11**

301 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLS 350  
 |||||  
 301 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLS 350  
 |||||  
 351 HHSAWLTVLEALEERPAVMTSPLYLEIIITYCTGAFLISCMVGSVIVYKMK 400  
 |||||  
 351 HHSAWLTVLEALEERPAVMTSPLYLEIIITYCTGAFLISCMVGSVIVYKMK 400  
 |||||  
 401 SGTKKSDFHQSOMAVHKLAKSIPLRRQVTVSADSSASMN SGVLLVRPSRLS 450  
 |||||  
 401 SGTKKSDFHQSOMAVHKLAKSIPLRRQVTVSADSSASMN SGVLLVRPSRLS 450  
 |||||  
 451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCGFQGVLAEAIGL 500  
 |||||  
 451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCGFQGVLAEAIGL 500  
 |||||  
 501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEM MMKMI GKHKNIINLLGA 550  
 |||||  
 501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEM MMKMI GKHKNIINLLGA 550  
 |||||

Fig. 11 (Cont.)

551 CTQDGPLYVIVEYASKGNLREYLOARRPPGLECYNPSHNPEEQSSKDL 600  
 |||||  
 551 CTQDGPLYVIVEYASKGNLREYLOARRPPGLECYNPSHNPEEQSSKDL 600  
 601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDEVNPKIADFGIARDIHH 650  
 |||||  
 601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDEVNPKIADFGIARDIHH 650  
 651 IDYKKTTNGRLPVKWMPEALFDRIYTHQSDVWSFGV 688  
 |||||  
 651 IDYKKTTNGRLPVKWMPEALFDRIYTHQSDVWSFGV 688

Fig. 11(Cont.)

2 PKRGKGAEDGDELRTPEAKSKTAAKKNDKEAAGEGALYEDPPDQ 51  
 1 PKRGKGAEDGDELRTPEAKSKTAAKKNDKEAAGEGALYEDPPDQ 50  
 52 KTSPSGKPATLKICSWNVVDGLRAWIKKKGLDWVKEEAPDILCLOETKCSE 101  
 51 KTSPSGKPATLKICSWNVVDGLRAWIKKKGLDWVKEEAPDILCLOETKCSE 100  
 102 NKLPaelQELPGLSHQYWSAPSDKEGYSGVGLLSRQCPLKVSYGI..... 146  
 101 NKLPaelQELPGLSHQYWSAPSDKEGYSGVGLLSRQCPLKVSYGIGDEEH 150  
 147 .....AYVPNAGRGLVRLRYRQWDEAFRFLKGLAS 178  
 151 DQEGRVIAEFDSEFVLVTAYVPNAGRGLVRLRYRQWDEAFRFLKGLAS 200  
 179 RKPLVLCGDLNVAHEEIDLNPKNKNAGFTPQERQCGFCELLQAVPLAD 228  
 201 RKPLVLCGDLNVAHEEIDLNPKNKNAGFTPQERQCGFCELLQAVPLAD 250

Fig. 12

229 SFRHLYPNTPYAYTEFTYMMNARSKNVGWRLDYFLSHSLIPALCDISKIR 278  
 |||||  
 251 SFRHLYPNTPYAYTEFTYMMNARSKNVGWRLDYFLSHSLIPALCDISKIR 300  
 |||||  
 279 SKALGSDHCPITLYLAL 295  
 |||||  
 301 SKALGSDHCPITLYLAL 317

Fig. 12(Cont.)



2 PKRGGKGAEDGDELRTGKMKALLPRNCGGVCHSLDVREPEAKSK 51  
 |||||  
 1 PKRGGKGAEDGDELRT.....EPEAKSK 26  
 52 TAAKNDKEAAGEGEPALYEDPPDQKTSFGKATLKICSWNVVDGLRAWIK 101  
 |||||  
 27 TAAKNDKEAAGEGEPALYEDPPDQKTSFGKATLKICSWNVVDGLRAWIK 76  
 102 KKGLDWVKEEAPDILCLQETKCSENKLPALQELPGLSHQYWSAPSDKEG 151  
 |||||  
 77 KKGLDWVKEEAPDILCLQETKCSENKLPALQELPGLSHQYWSAPSDKEG 126  
 152 YSGVGLLSRQCPLKVSYGIGDEEHDQEGRVIVAEFDSFVLVTAYVPNAGR 201  
 |||||  
 127 YSGVGLLSRQCPLKVSYGIGDEEHDQEGRVIVAEFDSFVLVTAYVPNAGR 176  
 202 GLVRLEYRQWDEAFRKFLKGLASRKPLVLCGLNVAHEEIDLNPKNK 251  
 |||||  
 177 GLVRLEYRQWDEAFRKFLKGLASRKPLVLCGLNVAHEEIDLNPKNK 226

Fig. 13

252 KNAGTPOERQGFCELLQAVPLADSFRLYPNTPIAYTFWTYMMNARSKN 301  
 |||  
 227 KNAGTPOERQGFCELLQAVPLADSFRLYPNTPIAYTFWTYMMNARSKN 276  
 |||  
 302 VGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPITLYLAL 342  
 |||  
 277 VGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPITLYLAL 317

Fig. 13(Cont.)



251 YSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFFTE 300  
 |||||  
 251 YSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFFTE 300

301 DEV 303

||.

301 DEL 303

**Fig. 14 (Cont.)**

1 MFQAAERPPQEWAMEGFKUGUHAHAAAA  
1 MFQAAERPPQEWAMEGPRDGLKXERLLDDRHDSGLDSMKDEEYEQMVVKELQ 50  
1 MFQAAERPPQEWAMEGPRDGLKXERLLDDRHDSGLDSMKDEEYEQMVVKELQ 100  
51 EIRLEPQEVPGRSEPWKOQLTEDGDSFLHLAIHEEKALTMVEIRQVKG 100  
51 EIRLEPQEVPGRSEPWKOQLTEDGDSFLHLAIHEEKALTMVEIRQVKG 150  
101 LAFTNFQNNIQQTPPLHLAVITNQPEIAEALLGAGCDPELDRFGNTPLHL 150  
101 LAFTNFQNNIQQTPPLHLAVITNQPEIAEALLGAGCDPELDRFGNTPLHL 183  
151 ACEQGCLASGVLTQSCTTPHLHSILKATNYG.....  
151 ACEQGCLASGVLTQSCTTPHLHSILKATNYGHTCLHLASHIGVLIVE 200  
151 ACEQGCLASGVLTQSCTTPHLHSILKATNYGHTCLHLASHIGVLIVE 222  
184 .....QEPCNGETALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250  
201 LLVLSLGADVNQAEPNGRGTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250

Fig. 15

223 YSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFTTE 272  
 |||||  
 251 YSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFTTE 300  
 |||||  
 273 DELPYDDCVFGGQRLTL 289  
 |||||  
 301 DELPYDDCVFGGQRLTL 317

Fig. 15 (Cont.)



[illegible]

Fig. 16 (Cont.)



601 TYEDPNQAVREFAKEIDASCIEKVIIGVEGFEVCSGLKVPGRKEICV 650  
 |||||  
 601 TYEDPNQAVREFAKEIDASCIEKVIIGVEGFEVCSGLKVPGRKEICV 650  
 651 AIKTLKAGYTDKQRDFLSEASIMGQFDHPNIIHLEGVVTKCKPVMITTE 700  
 |||||  
 651 AIKTLKAGYTDKQRDFLSEASIMGQFDHPNIIHLEGVVTKCKPVMITTE 700  
 701 YMENGSLDAFLRKNDGRFTVIQLVGMLRGIGSGMKYLSDMSYVHRDLAAR 750  
 |||||  
 701 YMENGSLDAFLRKNDGRFTVIQLVGMLRGIGSGMKYLSDMSYVHRDLAAR 750  
 751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTGGKIPIRWTAPEAIAYRK 800  
 |||||  
 751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTGGKIPIRWTAPEAIAYRK 800  
 801 FTSASDVWSYGIWMVEVMSYGERPYWDMSNQD ..... 832  
 |||||  
 801 FTSASDVWSYGIWMVEVMSYGERPYWDMSNQDVTKAIEEGYRLPPMDCP 850  
 833 .....PNT 835  
 |||  
 851 IALHQLMLDCWQKERSDRPKFGQIVNMMLDKLIRNPNSLKRGTGTESSRPNT 900

Fig. 16(Cont.)

```
836 ALLDPSSPEFSAVSVSGDWLQAIKMDRYKDNFVAAAG-ILLLJLVFVA *****  
|||||  
901 ALLDPSSPEFSAVSVSGDWLQAIKMDRYKDNFVTAAGTTLLEAVHVHNQED 950  
|||||
```

Fig. 16 (Cont.)

1 MNDFGKNDQVAPVANSYRCTLKQPAFTFDGSLFAVFPSSINEEQTLQ 50  
 1 MNDFGKNDQVAPVANSYRCTLKQPAFTFDGSLFAVFPSSINEEQTLQ 50  
 51 EVPTGLDSISHDSANCELP LLTPCSKAVMSQALKATFSGF ..... 90  
 51 EVPTGLDSISHDSANCELP LLTPCSKAVMSQALKATFSGFKEQRRLGIP 100  
 91 .....FWATNEFSLVNVNLFQFGMNGQMLCNLGKRFLEL 125  
 101 KNPWLWSEQVCQWLLWATNEFSLVNVNLFQFGMNGQMLCNLGKRFLEL 150  
 126 APDFVGDILWEHLEQMIKENQEKTEQYEENSHLTSPVPHWINSNTLGFGT 175  
 151 APDFVGDILWEHLEQMIKENQEKTEQYEENSHLTSPVPHWINSNTLGFGT 200  
 176 EQAPYGMQTONYPKGGLLDSMCPASTPSVLSSQEQFQMPKSRLLSSVST 225  
 201 EQAPYGMQTONYPKGGLLDSMCPASTPSVLSSQEQFQMPKSRLLSSVST 250  
 226 YCSVSQDFPGSNLLTNNSGTPKDHDSPENGADSFESSDILLQSWNSQS 275  
 251 YCSVSQDFPGSNLLTNNSGTPKDHDSPENGADSFESSDILLQSWNSQS 300

Fig. 17

276 SLDDVQVPSEFEDDCQSCLNKPTMSFKDYIQERSDPVEQKPVIP 325  
 |||||  
 301 SLDDVQVPSEFEDDCQSCLNKPTMSFKDYIQERSDPVEQKPVIP 350  
 |||||  
 326 AAVLAGFTGSGPIQLWQFLELLSDKSCQSFSISWTGDGWEFKLADPDEVA 400  
 |||||  
 351 AAVLAGFTGSGPIQLWQFLELLSDKSCQSFSISWTGDGWEFKLADPDEVA 425  
 |||||  
 376 RRWGKRKNKPKMNYEKLRSGLRYYDKNIIHKTS GKRYVYRFVCDLQNL 450  
 |||||  
 401 RRWGKRKNKPKMNYEKLRSGLRYYDKNIIHKTS GKRYVYRFVCDLQNL 450  
 426 GETPEELHAILGVQPD TED 444  
 |||||  
 451 GETPEELHAILGVQPD TED 469

Fig. 17 (Cont.)





```

301 YADWVPFQTKGLAPASAPQNLHAIRTDGSLLEWEVPEAPLEGLPGY 350
|||||
301 YADWVPFQTKGLAPASAPQNLHAIRTDGSLLEWEVPEAPLEGLPGY 350
|||||
351 KLSWQDNGTQDELTVEGTRANLTGWDPQKDLIVRCVSNVAVGCGPWSQP 400
|||||
351 KLSWQDNGTQDELTVEGTRANLTGWDPQKDLIVRCVSNVAVGCGPWSQP 400
|||||
401 LVVSSHDRAGQQGPPHSRTSWVPVLGVLTAALALILRRRKET 450
|||||
401 LVVSSHDRAGQQGPPHSRTSWVPVLGVLTAALALILRRRKET 450
|||||
451 RFGQAFDSVMARGEPAVHFRAARSFNRRPERIEATLDSLGISDELKEKL 500
|||||
451 RFGQAFDSVMARGEPAVHFRAARSFNRRPERIEATLDSLGISDELKEKL 500
|||||
501 EDVLIPEQOFTLGRMLGKEFGSVREAQLKQEDGSFVKVAVKMLKADIIA 550
|||||
501 EDVLIPEQOFTLGRMLGKEFGSVREAQLKQEDGSFVKVAVKMLKADIIA 550
|||||
551 SSDIEEFLREAACMKEFDHHPHAVKLVGVSLSRAKGRLPIMPVILPFMKH 600
|||||
551 SSDIEEFLREAACMKEFDHHPHAVKLVGVSLSRAKGRLPIMPVILPFMKH 600
|||||

```

Fig. 19 (Cont.)

601 GDLHAFLLASRIGENPFNLPLQTLIRFMVDIACGMEYLSRRNFIFHRDLAA 650  
 |||||  
 601 GDLHAFLLASRIGENPFNLPLQTLIRFMVDIACGMEYLSRRNFIFHRDLAA 650  
 |||||  
 651 RNCMLAEDMTVCVADFGLSRKIYSDCRY 678  
 |||||  
 651 RNCMLAEDMTVCVADFGLSRKIYSGDYY 678

Fig. 19 (Cont.)



Fig. 20

[illegible]

**Fig. 20 (Cont.)**

601 NAPQVLPQEAETCETPDNSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650  
 |||||  
 601 NAPQVLPQEAETCETPDNSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650  
 |||||  
 651 NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700  
 |||||  
 651 NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700  
 |||||  
 701 CQCDSNGDCTDVRIVGAGLGTGAI IAILLCIIILLILVLMFVVMKRRD 750  
 |||||  
 701 CQCDSNGDCTDVRIVGAGLGTGAI IAILLCIIILLILVLMFVVMKRRD 750  
 |||||  
 751 KERQAKQLLIDPEDDVRDNILKYDEEGGEEDQDYDLSQLQQPDTVEPDA 800  
 |||||  
 751 KERQAKQLLIDPEDDVRDNILKYDEEGGEEDQDYDLSQLQQPDTVEPDA 800  
 |||||  
 801 IKPVGIRRMDERPIHAEPQYFVRSAAAPHPGDIGDFINE 838  
 |||||  
 801 IKPVGIRRMDERPIHAEPQYFVRSAAAPHPGDIGDFINE 838  
 |||||

Fig. 20 (Cont.)



```

11 NVQILLEAASYLEQIEKENKCEHGYASSFSPMPRLQHSKPPRLSRA 60
   ||| ||| :||. |:| ||| ||| ||| ||| ||| ||| ||| |||
8 NVQRLLEAAEFLERRERE...CEHGYASSFSPMPRLQHSKPPRLSRA 54

61 QKHSSGSSNTSTANRSTHNELEKNRRAHLRLCLERLKVLIPLGPDCTRHT 110
   |||||. ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
55 QKHSSGTSNTSTANRSTHNELEKNRRAHLRLCLERLKVLIPLGPDCTRHT 104

111 TLGLLNKAKAHIKLEEAERKSQHOLENLEREQRFLKWRLEQLQGPOEME 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
105 TLGLLNKAKAHIKLEEAERKSQHOLENLEREQRFLKWRLEQLQGPOEME 154

161 RIRMDSIGSTISSDRSDSREEIEVDVESTEFSHGEVDNISTSIDIDD 210
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
155 RIRMDSIGSTISSDRSDSREEIEVDVESTEFSHGEVDNISTSIDIDD 204

211 HSSLPSIGSDEGYSSASVKLSFTS 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
205 HSSLPSIGSDEGYSSASVKLSFTS 228

```

Fig. 22

```

1 MESPASSQPASMPQSGKSKRKDLRISCMKPPAPNTPPRNLDSTFI 50
  |||||
1 MESPASSQPASMPQSGKSKRKDLRISCMKPPAPNTPPRNLDSTFI 50
  |||||

51 TIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTMAVKRIRATVN 100
  |||||
51 TIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTMAVKRIRATVN 100
  |||||

101 SEQKRLMLDLINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKF 150
  |||||
101 SEQKRLMLDLINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKF 150
  |||||

151 YRKVLDKNMTIPEDILGEIAVSIVRALEHLHSLSVIHRDVKPSNVLINK 200
  |||||
151 YRKVLDKNMTIPEDILGEIAVSIVRALEHLHSLSVIHRDVKPSNVLINK 200
  |||||

201 EGHVKMCDFGISGYLVDVSVAKTMDAGCKPYMAPERINPELNQKGYNVKSD 250
  |||||
201 EGHVKMCDFGISGYLVDVSVAKTMDAGCKPYMAPERINPELNQKGYNVKSD 250
  |||||

```

Fig. 23

251 VWSLGITMIEMAILRFPYESWGTFQQLKQVVVEEPPQLPADRFSPFVD 300  
 |||||  
 251 VWSLGITMIEMAILRFPYESWGTFQQLKQVVVEEPPQLPADRFSPFVD 300  
 |||||  
 301 FTAQCLRKNEAERMSYLELI 320  
 |||||  
 301 FTAQCLRKNEAERMSYLEIM 320

Fig. 23(Cont.)





```

1 MPEIRLRHVVCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISSVVLQLE 50
  |||||
1 MPEIRLRHVVCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISSVVLQLE 50
  |||||
51 KEEQIHSVDIGNDGSFVEVLVGSAGGAGEQDYEVLLVTSSFMSPSESR 100
  |||||
51 KEEQIHSVDIGNDGSFVEVLVGSAGGAGEQDYEVLLVTSSFMSPSESR 100
  |||||
101 SGSNPNRVRMFGDPKLVRAAAEKRWDRVKIVCSQPYSKDSPPFGLSFVRFH 150
  |||||
101 SGSNPNRVRMFGDPKLVRAAAEKRWDRVKIVCSQPYSKDSPPFGLSFVRFH 150
  |||||
151 SPPDKDEAEAPSQKVTVTKLQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||||
151 SPPDKDEAEAPSQKVTVTKLQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||||
201 VTASDPAGPSYAAATLQASSAASSASPVSRRAIGSTSKPQESS.....DF 244
  |||||
201 VTASDPAGPSYAAATLQASSAASSASPVSRRAIGSTSKPQESPKGKRKLDL 250
  |||||
245 GGVEEERSWRPQSIPIPSAP 264
  ||..:|.|||
251 NQEEKKTPSKPPAQLSPSVP 270

```

Fig. 25

```

1 MPEIRLHVVCSSQDSTHCAENLLKADTYRKWRAAKAGEKTSVVVLQLE 50
|||||
1 MPEIRLHVVCSSQDSTHCAENLLKADTYRKWRAAKAGEKTSVVVLQLE 50
|||||
51 KEEQIHSVDIGNDGSFAFVELVGCSSAGGAGEQDYEVLVTSFMSPSER 100
|||||
51 KEEQIHSVDIGNDGSFAFVELVGCSSAGGAGEQDYEVLVTSFMSPSER 100
|||||
101 SCSNPNVRVMFGPKLVRAAAEKWRDVKIVCSQPYSKDSPFGLSFVRFH 150
|||||
101 SCSNPNVRVMFGPKLVRAAAEKWRDVKIVCSQPYSKDSPFGLSFVRFH 150
|||||
151 SPDKDEAAEPSQKVTVKLGQFRVKEEDESANSLRLEDYMSDRVQFV.. 198
|||||
151 SPDKDEAAEPSQKVTVKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200
|||||
199 ITAQE.WDPSFEEALMDNPSIA 219
:|: |:|: |:|
201 VTASDPAGESYAAATIQASSAA 222

```

**Fig. 26**

```

1 MPEIRLHVVCSSQDSTHCAENLLKADTYRKWRAAKAGEKTI SVVLQLE 50
  |||||
1 MPEIRLHVVCSSQDSTHCAENLLKADTYRKWRAAKAGEKTI SVVLQLE 50
  |||||
51 KEEQIHSV DIGNDGS AFVEVLVGSSAGGAGEQYEVLLVTSSFMSPSESR 100
  |||||
51 KEEQIHSV DIGNDGS AFVEVLVGSSAGGAGEQYEVLLVTSSFMSPSESR 100
  |||||
101 SGSNPNRVRMFGPDKLVRAAAAEKRWDRVKIVCSQPYSKDSPFGLSFVRFH 150
  |||||
101 SGSNPNRVRMFGPDKLVRAAAAEKRWDRVKIVCSQPYSKDSPFGLSFVRFH 150
  |||||
151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||||
151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||||
201 VTASDPAGPSYAAATLQASSAASSASPVSRRAIGSTSKPQESP KGRKLDL 250
  |||||
201 VTASDPAGPSYAAATLQASSAASSASPVSRRAIGSTSKPQESP KGRKLDL 250
  |||||
251 NQEEKKTPSKPPAQLSPSVPRPKLPAPTRTPATAVPARAQGA VTGKPR 300
  |||||
251 NQEEKKTPSKPPAQLSPSVPRPKLPAPTRTPATAVPARAQGA VTGKPR 300
  |||||

```

Fig. 27



[illegible]

Fig. 28

301 CIGNHDLFMRRRKADSLEVOQKAQAREEKARK..... 333  
 |||||  
 300 CIGNHDLFMRRRKADSLEVOQKAQAREEKARKOMERQRLAREKOMREEA 349  
 334 .....QMKEEATMANEALMRSEETADLLAEKAQITEEEAKLLA 371  
 |||||  
 350 ERTRDELEERRLLQMKEEATMANEALMRSEETADLLAEKAQITEEEAKLLA 399  
 372 QKAAEAQEMQRIKATAIRTEEEKRIMEQKVLEAEVLALKMAEESERRAK 421  
 |||||  
 400 QKAAEAQEMQRIKATAIRTEEEKRIMEQKVLEAEVLALKMAEESERRAK 449  
 422 EADQLKQDLQEAAREARRAKQKLEIATKPTYPPMNPPIAPLPDIPSN 471  
 |||||  
 450 EADQLKQDLQEAAREARRAKQKLEIATKPTYPPMNPPIAPLPDIPSN 499  
 472 LIGDSLSTFDKDTMKRLSMEIEKEKVEYMEKSKHLQEQNLNELKTEIEAL 521  
 |||||  
 500 LIGDSLSTFDKDTMKRLSMEIEKEKVEYMEKSKHLQEQNLNELKTEIEAL 549  
 522 KLKERETALDILHNENSDRGSSKHNTIKKLTILQSAKSRVAFEEEL 567  
 |||||  
 550 KLKERETALDILHNENSDRGSSKHNTIKKLTILQSAKSRVAFEEEL 595

Fig.28 (Cont.)

```

1 MRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVFGY 50
  |||||
1 MRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVFGY 50
  |||||
51 ASLLCNLIGFGYPAYISIKAIESPKNKDDTQWLTYWVYGVFSIAEFFSD 100
  |||||
51 ASLLCNLIGFGYPAYISIKAIESPKNKDDTQWLTYWVYGVFSIAEFFSD 100
  |||||
101 IFLSWFPFYMLK 113
  |||||
101 IFLSWFPFYMLK 113
  |||||

```

Fig. 29

```

1 MDLEGRNGGAKKKNFKLNKSEKDKKPTVSVFSMFYSYNWLDKLY 50
|||||
1 MDLEGRNGGAKKKNFKLNKSEKDKKPTVSVFSMFYSYNWLDKLY 50
|||||

51 MVVGTIAAIHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSND 100
|||||
51 MVVGTIAAIHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSND 100
|||||

101 TGFFMNLEEDMTRYAYYSYGIGAGLVAAAYIQVSFWCLAAGRQIHKIRKQ 150
|||||
101 TGFFMNLEEDMTRYAYYSYGIGAGLVAAAYIQVSFWCLAAGRQIHKIRKQ 150
|||||

151 FFHAIMRQEIGWFDVHDVGEINTRLTDDVSKINEVIGDKIGMFFQSMATF 200
|||||
151 FFHAIMRQEIGWFDVHDVGEINTRLTDDVSKINEVIGDKIGMFFQSMATF 200
|||||

201 FTGFTVGFTRGWKLTIVILATSPVLGLSAAVWAKILSSFTDKELLAYAKA 250
|||||
201 FTGFTVGFTRGWKLTIVILATSPVLGLSAAVWAKILSSFTDKELLAYAKA 250
|||||

251 GAVAEVLAAIRTVIAFGGQKELERYNKNLEEAKRIGIKKAITANISIG 300
|||||
251 GAVAEVLAAIRTVIAFGGQKELERYNKNLEEAKRIGIKKAITANISIG 300
|||||

```

Fig. 30



301	AAFLLIYASYALAFWYGTTTLVLSGEYSICQVLTVFFSVLIGAFSVGQASP	350
301	AAFLLIYASYALAFWYGTTTLVLSGEYSICQVLTVFFSVLIGAFSVGQASP	350
351	SIEAFANARGAAVEIFKIIDNKPIDSYSKSGHKPDNIKNLEFRNVHFS	400
351	SIEAFANARGAAVEIFKIIDNKPIDSYSKSGHKPDNIKNLEFRNVHFS	400
401	YPSRKEVKILKGNLKVQSGQTVALVNSGCGKSTTVQLMQRLYDPTGEM	450
401	YPSRKEVKILKGNLKVQSGQTVALVNSGCGKSTTVQLMQRLYDPTGEM	450
451	VSVDGQDIRTINVRFLREIIGVVSQEPVLFTTIAENIRYGRENVTMDEI	500
451	VSVDGQDIRTINVRFLREIIGVVSQEPVLFTTIAENIRYGRENVTMDEI	500
501	EKAVKEANAYDFTMKLPKHFDTLVGERGAQLSGGQKORIAIARALVRNPK	550
501	EKAVKEANAYDFTMKLPKHFDTLVGERGAQLSGGQKORIAIARALVRNPK	550
551	ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVITAG	600
551	ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVITAG	600

**Fig. 30 (Cont.)**

601	FDDGVIVEKGNHDELMKEGIYFKLVTMTQAGNEVELENAADESKSEIDA	650
601	FDDGVIVEKGNHDELMKEGIYFKLVTMTQAGNEVELENAADESKSEIDA	650
651	LEMSSNDSRSSLIRKRSTRBSVRGSQAQRKLSKTEALDESIPPVSFWRI	700
651	LEMSSNDSRSSLIRKRSTRBSVRGSQAQRKLSKTEALDESIPPVSFWRI	700
701	MKLNLTWPYFVGVFCAIINGGLQPAFAIIFSKIIGVTRIDDPETKRQ	750
701	MKLNLTWPYFVGVFCAIINGGLQPAFAIIFSKIIGVTRIDDPETKRQ	750
751	NSNLFSLFLALGIIISFITFFIQGFTFGKAGEILTKRLRYMVFRSMLRQD	800
751	NSNLFSLFLALGIIISFITFFIQGFTFGKAGEILTKRLRYMVFRSMLRQD	800
801	VSWFDDPKNTTGALTTRLANDAAQVKGATCSRLAVITQNIANLGTGIIIS	850
801	VSWFDDPKNTTGALTTRLANDAAQVKGATCSRLAVITQNIANLGTGIIIS	850
851	FIYGWQITLILLALVIPPIAAGVYEMKMLSQALKDKKELEGAGKIATEA	900
851	FIYGWQITLILLALVIPPIAAGVYEMKMLSQALKDKKELEGAGKIATEA	900

**Fig. 30 (Cont.)**

901 IENFRTVVSILTQEQKFEHMYAQSLQVPRNSLRKAHIFGITFTSQAMMY 950  
 IENFRTVVSILTQEQKFEHMYAQSLQVPRNSLRKAHIFGITFTSQAMMY 950  
 901 IENFRTVVSILTQEQKFEHMYAQSLQVPRNSLRKAHIFGITFTSQAMMY 950  
 IENFRTVVSILTQEQKFEHMYAQSLQVPRNSLRKAHIFGITFTSQAMMY 950  
 951 FSYAGCFRFGAYLVAHKLMSFEDVLLVFSVAVFGAMAVGQVSSFAPDYAK 1000  
 FSYAGCFRFGAYLVAHKLMSFEDVLLVFSVAVFGAMAVGQVSSFAPDYAK 1000  
 951 FSYAGCFRFGAYLVAHKLMSFEDVLLVFSVAVFGAMAVGQVSSFAPDYAK 1000  
 FSYAGCFRFGAYLVAHKLMSFEDVLLVFSVAVFGAMAVGQVSSFAPDYAK 1000  
 1001 AKISAAHIIMIIEKTPLIDSYSYSTEGLMPNTLEGNVTFGEVVFNYPTRPDI 1050  
 AKISAAHIIMIIEKTPLIDSYSYSTEGLMPNTLEGNVTFGEVVFNYPTRPDI 1050  
 1001 AKISAAHIIMIIEKTPLIDSYSYSTEGLMPNTLEGNVTFGEVVFNYPTRPDI 1050  
 AKISAAHIIMIIEKTPLIDSYSYSTEGLMPNTLEGNVTFGEVVFNYPTRPDI 1050  
 1051 PVLQGLSLEVKKGTALVCGSSCGKSTVVQLLERYDPLAGKVLLDGKE 1100  
 PVLQGLSLEVKKGTALVCGSSCGKSTVVQLLERYDPLAGKVLLDGKE 1100  
 1051 PVLQGLSLEVKKGTALVCGSSCGKSTVVQLLERYDPLAGKVLLDGKE 1100  
 PVLQGLSLEVKKGTALVCGSSCGKSTVVQLLERYDPLAGKVLLDGKE 1100  
 1101 IKRLNVQWLR AHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK 1150  
 IKRLNVQWLR AHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK 1150  
 1101 IKRLNVQWLR AHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK 1150  
 IKRLNVQWLR AHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK 1150  
 1151 EANHAFIESLPNKYSTKVGDKGTLQSLGGKQRTAARALVRQPHILLD 1200  
 EANHAFIESLPNKYSTKVGDKGTLQSLGGKQRTAARALVRQPHILLD 1200  
 1151 EANHAFIESLPNKYSTKVGDKGTLQSLGGKQRTAARALVRQPHILLD 1200  
 EANHAFIESLPNKYSTKVGDKGTLQSLGGKQRTAARALVRQPHILLD 1200

1201 EATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIIVFQNGR 1250  
 |||||  
 1201 EATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIIVFQNGR 1250  
 |||||  
 1251 VKEHGTHQQLLAQKGIYFSMVSVQAGT 1277  
 |||||  
 1251 VKEHGTHQQLLAQKGIYFSMVSVQAGT 1277

Fig. 30(Cont.)

```

1 MDLEGRNGGAKKNFFKLNKSEKDKEKKPTVSFMSFRYSNWLDKLY 50
| | | | | | | | | | | | | | | | | | | | | | | | | |
1 MDLEGRNGGAKKNFFKLNKSEKDKEKKPTVSFMSFRYSNWLDKLY 50

51 MUVGTAAIIHGAGLPIMLLVFGEMTDIFANAGNLEDLMSNITNRSDIND 100
| | | | | | | | | | | | | | | | | | | | | | | | | |
51 MUVGTAAIIHGAGLPIMLLVFGEMTDIFANAGNLEDLMSNITNRSDIND 100

101 TGFFMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAAGROIHKIRKQ 150
| | | | | | | | | | | | | | | | | | | | | | | | | |
101 TGFFMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAAGROIHKIRKQ 150

151 FFHAI MRQEIGFDVHDVGELNTRLTDDVSKINEGIGDKIGMFFQSMA TF 200
| | | | | | | | | | | | | | | | | | | | | | | | | |
151 FFHAI MRQEIGFDVHDVGELNTRLTDDVSKINEGIGDKIGMFFQSMA TF 200

201 FTGTFIVGFTRGWKLTLVILATSPVLGLSAAVWAKILSSFTDKELLAYAKA 250
| | | | | | | | | | | | | | | | | | | | | | | | | |
201 FTGTFIVGFTRGWKLTLVILATSPVLGLSAAVWAKILSSFTDKELLAYAKA 250

251 GAVAHEVLA AIRT V IAFGGOKKELERYNK NLEEAKRIGIKKAITANISIG 300
| | | | | | | | | | | | | | | | | | | | | | | | | |
251 GAVAHEVLA AIRT V IAFGGOKKELERYNK NLEEAKRIGIKKAITANISIG 300

```

Fig. 31

```

301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFSVLIGAFSVGQASP 350
|||||
301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFSVLIGAFSVGQASP 350
|||||
351 SIEAFANARGAAAYEIFKIIDNKPSIDSYKSGHKPDNIKGNLEFRNVHFS 400
|||||
351 SIEAFANARGAAAYEIFKIIDNKPSIDSYKSGHKPDNIKGNLEFRNVHFS 400
|||||
401 YPSRKEVKILKGLNLKVQSGQTVALVGNSSGCGKSTTVQLMQRLYDPTGEM 450
|||||
401 YPSRKEVKILKGLNLKVQSGQTVALVGNSSGCGKSTTVQLMQRLYDPTGEM 450
|||||
451 VSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500
|||||
451 VSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500
|||||
501 ERKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIAIARALVRNPK 550
|||||
501 ERKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIAIARALVRNPK 550
|||||
551 IILLDEATSALDTESEAEVQAALDKVSR 578
|||||
551 IILLDEATSALDTESEAVVQVALDKARK 578
|||||

```

Fig. 31(Cont.)



```

1 MSRSKRDNFNYSVEIGDSTFTVLKRYQNLKPIGSAGQGIVCAAYDAIHR 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MSRSKRDNFNYSVEIGDSTFTVLKRYQNLKPIGSAGQGIVCAAYDAIHR 50

1 NVAIKKLSPFQOQTHAKRAYRELVLVKVCVNHKNIIGLLNVFTPQKSLEE 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 NVAIKKLSPFQOQTHAKRAYRELVLVKVCVNHKNIIGLLNVFTPQKSLEE 100

1 FQDYIVMELMDANLCQVIQMELDHERSYLLYQMLCGIKHLHSAGIIHR 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 FQDYIVMELMDANLCQVIQMELDHERSYLLYQMLCGIKHLHSAGIIHR 150

1 DLPSNIVVKS DCTLKILDGLARTAGTSFMTPYVVTRY YRAPEVILGM 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 DLPSNIVVKS DCTLKILDGLARTAGTSFMTPYVVTRY YRAPEVILGM 200

201 GYKENVDLSVG CIMGEMVCHILFPGRDYIDQWNKVIEQLGTPCPPEFMK 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 GYKENVDLSVG CIMGEMVCHILFPGRDYIDQWNKVIEQLGTPCPPEFMK 250

      251 KLQPTWRTYVENRPKYAGSYFEKLPDPDLFPADSEHNKLKASQ 293
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      251 KLQPTWRTYVENRPKYAGSYFEKLPDPDLFPADSEHNKLKASQ 293

```

**Fig. 33**



1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSAQGIVCAAYDAILER 50  
 1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSAQGIVCAAYDAILER 50  
 51 NVAIKKLSRPFQNHAKRAYRELVLKMCVNHKNIIIGLLNVFTPOKSLEE 100  
 51 NVAIKKLSRPFQNHAKRAYRELVLKMCVNHKNIIIGLLNVFTPOKSLEE 100  
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIHR 150  
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIHR 150  
 151 DLKPSNIVVKS DCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200  
 151 DLKPSNIVVKS DCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200  
 201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPPEFMK 250  
 201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPPEFMK 250

Fig. 34

```

251 KIQTVRTYVENRPKYAGYSFEKLFDPVLFPADSEHNKLIKASQARDLLSK 300
|||||
251 KIQTVRTYVENRPKYAGYSFEKLFDPVLFPADSEHNKLIKASQARDLLSK 300
|||||
301 MLVIDASKRISVDEALQHPYINWYDPSEAEARSCKL 337
|||||
301 MLVIDASKRISVDEALQHPYINWYDPSEAEAPPKI 337
|||||

```

**Fig. 34(Cont.)**



```

1 MSPFTRIGLSNFDGSCQCGEAVNPYCAVLVKEYVESENGOMYIQKKP 50
  |||||
1 MSPFTRIGLSNFDGSCQCGEAVNPYCAVLVKEYVESENGOMYIQKKP 50
  |||||
51 TMYPPWDSTFDAHINKGRVMQIIVKGKNVDLISSETVELYSLAERCCKNN 100
  |||||
51 TMYPPWDSTFDAHINKGRVMQIIVKGKNVDLISSETVELYSLAERCCKNN 100
  |||||
101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFETEGFFALHQRGAIK 150
  |||||
101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFETEGFFALHQRGAIK 150
  |||||
151 QAKVHVVKCHEFTATFFPQPTFCVCHFEFVWGLNKQGYQCRQCNAAIHKK 200
  |||||
151 QAKVHVVKCHEFTATFFPQPTFCVCHFEFVWGLNKQGYQCRQCNAAIHKK 200
  |||||
201 CIDKVIACKTGSAINSRETMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250
  |||||
201 CIDKVIACKTGSAINSRETMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250
  |||||

```

Fig. 36

251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINQKIMAEALAMTESTQQ 300  
 |||||  
 251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINQKIMAEALAMTESTQQ 300  
 301 ARCLRDTEQIFREGPVEIGLPCSIKNEARPPCLPTPGKREPQGISWESPL 350  
 |||||  
 301 ARCLRDTEQIFREGPVEIGLPCSIKNEARLPCLPTPGKREPQGISWESPL 350  
 351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFGKVFLAEFK 400  
 |||||  
 351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFGKVFLAEFK 400  
 401 KTNQFFAIFALKKDVVIMDDDDVECTMVEKRVLSLAWHPFLTHMFCTFQT 450  
 |||||  
 401 KTNQFFAIFALKKDVVIMDDDDVECTMVEKRVLSLAWHPFLTHMFCTFQT 450  
 451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGLQFLHSGKI 500  
 |||||  
 451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGLQFLHSGKI 500

Fig. 36 (Cont.)

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501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550
|||||
501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550
|||||
551 LLGQKYNHSVDWWSFGVLLYEMLIGQSPFHGQDEEELFHSIRMDNPFYPR 600
|||||
551 LLGQKYNHSVDWWSFGVLLYEMLIGQSPFHGQDEEELFHSIRMDNPFYPR 600

        601 WLEKEAKDLLVK..VRSEAKSVFIR 623
            |||||
        601 WLEKEAKDLLVKLFVREPEKRLGVR 625

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**Fig. 36 (Cont.)**